

REMARKS

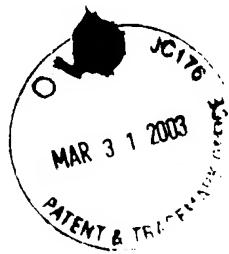
The Office Action has required restriction, under 35 U.S.C. §121, to either claims 1, 2 and 12-18 (Group I), allegedly drawn to an amplification method for detecting fungus, or claims 3-11 (Group II), allegedly drawn to a primer and probe set. The Office Action has further required restriction between the sequence identification numbers consisting of SEQ. ID. Nos. 1, 2 and 5 or SEQ. ID. Nos. 3, 4 and 5 to be examined with the corresponding elected Group I or II.

In response to the restriction requirement, Applicants elect the claims of Group I and the sequence identification numbers consisting of SEQ. ID. Nos. 1, 2 and 5. In accordance with this election, Applicants have amended claims 1 and 12 to remove SEQ. ID. Nos. 3 and 4. Consistent with this election, Applicants believe that claims 1-2, 12-15 and 18 should now be the subject of further examination. Applicants reserve the right to file a divisional application(s) directed to the non-elected subject matter. If any questions remain, the Examiner is invited to contact the undersigned at the telephone number listed below.

Respectfully submitted,

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U.S. Patent Application No. 10/080,959
Attorney's Docket No. 0001-00001

MARKED-UP VERSION OF AMENDMENT SHOWING CHANGES MADE

Claims 1 and 12 have been amended as follows:

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1. (Amended) A method for detecting the fungus *Stachybotrys chartarum*, comprising:
 - isolating DNA from a sample suspected of containing the fungus *Stachybotrys chartarum*;
 - subjecting the DNA to polymerase chain reaction amplification utilizing at least one primer, wherein the at least one primer comprises one of a (SEQ. ID NO. 1)
5'GTTGCTTCGGCGGGAAC3'][,] and (SEQ. ID NO. 2)
5'TTTGCCTTGCCACTCAGAG3'][, (SEQ. ID NO. 3) 5'ACCTATCGTGTTCGGCG3',
and (SEQ. ID NO. 4) 5'GCGTTGCCACTCAGAGAATACT3'] base sequence; and
 - detecting the fungus *Stachybotrys chartarum* by visualizing the product of the polymerase chain reaction.

12. (Amended) A method for detecting the presence of the fungus *Stachybotrys chartarum*, comprising:
 - obtaining a sample from the environment;
 - extracting DNA from the sample; and
 - amplifying the extracted DNA by polymerase chain reaction utilizing one or more

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5'GTTGCTTCGGCGGGAAC3'][,] and (SEQ. ID NO. 2)

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5'TTTGCCTTGCCACTCAGAG3'][, (SEQ. ID NO. 3) 5'ACCTATCGTTGCTTCGGCG3',
and (SEQ. ID NO. 4) 5'GCGTTGCCACTCAGAGAATACT3'] base sequence.